

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 05:12:55 ; Search time 1602.78 Seconds
(without alignments)
9027.275 Million cell updates/sec

Title: US-09-811-118-2

Perfect score: 1072
Sequence: 1 GACGCCGCCACCTCGGAC.....TTGCATCCACATGAATTTC 1072

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapept 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	621	57.9	1011	9	AL543692 AL543692
2	577	53.8	961	9	AL543655 AL543655
3	553	51.6	936	10	BI905842 BI905842
4	531	49.5	760	10	BI550170 BI550170
5	524	48.9	625	9	AW957082 AW957082
6	502	46.8	617	10	BE383506 BE383506
7	468	43.7	519	9	AA406605 AA406605
8	465	43.4	534	10	BE314194 BE314194
9	452	42.2	466	9	AI635816 AI635816
10	452	42.2	852	9	AL554204 AL554204
11	437	40.8	846	10	BI561449 BI561449
12	419	39.1	465	9	AI925364 AI925364
13	409	38.2	464	9	AW576111 AW576111
14	404	37.7	456	9	AA599283 AA599283
15	400	37.3	466	9	AI332841 AI332841
16	399	37.2	436	9	AA557291 AA557291
17	388	36.2	894	10	BI767772 BI767772

C 18	370	34.5	382	9	AW195935	AW195935	xl85a05.x
C 19	351	32.7	397	9	AI376136	AI376136	ta59c04.x
C 20	349	32.6	436	9	AI094047	AI094047	qa28f09.s
C 21	347	32.4	367	9	AA722806	AA722806	z981g08.s
C 22	346	32.3	403	9	AA405247	AA405247	UI-HF-BL0
C 23	340	31.7	450	9	AA815259	AA815259	a164d10.s
C 24	339	31.6	453	9	AI093865	AI093865	qa30e01.s
C 25	338	31.5	426	9	AA778372	AA778372	z156h05.s
C 26	337	31.4	399	9	AA736389	AA736389	x015e01.x
C 27	330	30.8	524	10	BE856755	BE856755	7f68c12.x
C 28	328	30.6	447	9	AI199140	AI199140	q146f11.x
C 29	327	30.5	327	9	BE047114	BE047114	hg64g08.x
C 30	327	30.5	454	10	BE646553	BE646553	7e91h09.x
C 31	325	30.3	419	9	AA777994	AA777994	z4f4c03.s
C 32	321	29.9	423	10	AA7086	AA7086	zc43e03.r1
C 33	314	29.3	405	10	BI110030	BI110030	7n45b05.x
C 34	312	28.1	366	9	AM135756	AM135756	UI-H-BL1
C 35	310	28.9	542	9	AA959644	AA959644	EST371714
C 36	296	27.6	547	9	AA749209	AA749209	ny11h09.s
C 37	239	22.3	435	9	AA992639	AA992639	ot81b11.s
C 38	232	21.6	356	9	AI401448	AI401448	tg64b11.x
C 39	227	21.2	720	10	BT772530	BT772530	60305444
C 40	217	20.2	390	10	BE900356	BE900356	H0A37-1-G
C 41	216	20.1	392	10	BE900355	BE900355	H0A37-1-G
C 42	210	19.6	411	9	AA700564	AA700564	z134b10.s
C 43	200	18.7	331	9	AA975019	AA975019	on59e06.s
C 44	195	18.2	238	9	AA592186	AA592186	hf47c06.x
C 45	194	18.1	465	9	AI312116	AI312116	qp89c08.x

ALIGNMENTS

RESULT 1
AL543692 1011 bp mRNA linear EST 16-FEB-2001
LOCUS AL543692 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1006YD22 5
DEFINITION AL543692 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1006YD22 5
prime, mRNA sequence.
ACCESSION AL543692
VERSION AL543692.1 GI:12876171
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1011)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
COMMENT
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1. 1011

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1006YD22"
/clone_1lb="LTI_NFL006_PL2"

/ribose_type="piacenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 251 a 279 c 262 g 217 t 2 others
ORIGIN

Query Match	57.9%;	Score 621;	DB 9;	Length 1011;
Best Local Similarity	99.6%;	Pred. No. 1.9e-309;		
Matches 891;	Conservative	0;	Mismatches 3;	Indels 1;
				Gaps 1

OY	87	AGAGCAGAGACTTCTACGACTTCGAAGCGGTCACAACTCCGGGGCAAACTGTTGGTGG	149
Db	76	AGAGCAGAGACTTCTACGACTTCAAGCGGTCACAACTCCGGGGCAAACTGTTGGTGG	135
OY	147	AGAGATACCCGGGATCGGTGTCCTCGTGTGTAATGTGGCAGCAGTCCGGCTTCCACAG	206
Db	136	AGAGATACCCGGGATCGGTGTCCTCGTGTGTAATGTGGCAGCAGTCCGGCTTCCACAG	195
OY	207	ACCAAGCACTACCGAGCCCTGACAGGTGAGCGAAGCACTGGGGCCCCACCACTTCAAG	266
Db	196	ACCAAGCACTACCGAGCCCTGACAGGTGAGCGAAGCACTGGGGCCCCACCACTTCAAG	255
OY	267	TGCTGCGCTTCCCTGCAACCAAGTTGGCCACAGAGCCTGCACGACCAAGAGATTGG	326
Db	256	TGCTGCGCTTCCCTGCAACCAAGTTGGCCACAGAGCCTGCACGACCAAGAGATTGG	315
OY	327	AGAGCTTGGCTGGCCGCAACCAAGTGTCTCATTTCCCATGTTTACCAAGATTGCAGTCA	386
Db	316	AGAGCTTGGCCCGCCGCAACCAAGTGTCTCATTTCCCATGTTTACCAAGATTGCAGTCA	375
OY	387	CCGAGTACGTGGCCATCTGCTTCAAGTACCTGGGCCAGACTTCTGGAAAGAGCCCA	446
Db	376	CCGAGTACGTGGCCATCTGCTTCAAGTACCTGGGCCAGACTTCTGGAAAGAGCCCA	435
OY	447	CCTGGAACCTTTCGAAGTACTAGTACCCCAATGGAAGGTGTGAAGGGCTTGGGAGCC	506
Db	436	CCTGGAACCTTTCGAAGTACTAGTACGCCCAATGGAAGGTGTGAAGGGCTTGGGAGCC	495
OY	507	CAAGCTGTCAAGTGAAGAGGTCAAGACTCCAGATCACAGGCGCTCGTAGGAAGCTCATCC	566
Db	496	CAAGCTGTCAAGTGAAGAGGTCAAGACTCCAGATCACAGGCGCTCGTAGGAAGCTCATCC	555
OY	567	TACTGAAGCGAAGACTTATPACCAACCGCGCTCTCTCTCACACCCTATCCCCGCCA	626
Db	556	TACTGAAGCGAAGACTTATPACCAACCGCGCTCTCTCTCACACCCTATCCCCGCCA	615
OY	627	CCGTGTGGGGGTGACCAATGCAACTCAATGTGGCTCCAAAGGAGAGACCACACTGAC	686
Db	616	CCGTGTGGGGGTGACCAATGCAACTCAATGTGGCTCCAAAGGAGAGACCACACTGAC	675
OY	687	TCCTCTTCTTACTCTTATGCCATTTGGTCCATCTTCTTGTGGGGAAAAATTCTAGT	746
Db	676	TCCTCTTCTTACTCTTATGCCATTTGGTCCATCTTCTTGTGGGGAAAAATTCTAGT	735
OY	747	ATTTTGATTTATTTGAATCTTACAGCAACAATPAGAACTCTCGGCCAATGAG	805
Db	736	ATTTTGATTTATTTGAATCTTACAGCAACAATPAGAACTCTCGGCCAATGAGAGCTTT	795
OY	806	GACCACTGATACCAAGCGGATACCAAGCTGTGGCAACAATAATGTGTGGCAATAGAA	865
Db	796	GACCACTGATACCAAGCGGATACCAAGCTGTGGCAACAATAATGTGTGGCAATAGAA	855
OY	866	GTAATATCAAGCAATAATCTCCACCAAGGCTTCTGTAACTGGGACCAATGATTACTC	922
Db	856	GTAATATCAAGCAATAATCTCCACCAAGGCTTCTGTAACTGGGACCAATGATTACTC	915
OY	926	ATAGGGCTGTGTGAGAGATTAGAGTAATTCCTGTGAAGGCGCTAGGAGGTGC	980
Db	916	ATAGGGCTGTGTGAGAGATTAGAGTAATTCCTGTGAAGGCGCTAGGAGGTGC	970

RESULT	2
AL543655/c	
LOCUS	961 bp mRNA linear EST 16-FEB-2001
DEFINITION	AL543655 LTI_NFL006.PL2 Homo sapiens CDNA clone CSODI006YD22 3
ACCSSION	prime,mRNA sequence.
VERSION	AL543655 AL543655.1 GT:12876134

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 961)
TITLE	Li, W.B., Gruber, C., Jesse, J., and Polares, D.
JOURNAL	Full-length cDNA libraries and normalization
COMMENT	Unpublished (2001)
FEATURES	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: secre@genoscope.cns.fr , Web : www.genoscope.cns.fr .
SOURCE	Location/Qualifiers 1..961

FEATURES	SOURCE	Location/Qualifiers
BASE COUNT	231	1..961
ORIGIN	a	/organism="Homo sapiens"
	207	/db_xref="taxon:9606"
	c	/clone="CSOD1006YD2"
	252	/clone_1ib="Lri_NFL006_PL2"
	g	/tissue_type="Placenta"
	267	/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
	t	was primed with a NotI-oligo(dT) primer. Five prime end
	4	enriched, double-stranded cDNA was digested with Not I and
	others	cloned into the Not I and Eco RV sites of the pCMVSPORT 6
		vector. Library was normalized. Library was constructed by
		life Technologies. Contact : Feng Liang Life Technologies
		a division of Invitrogen 9800 Medical Center Drive
		Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
		Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

Query Match	53.8%	Score 577;	DB 9;	Length 961;
Best Local Similarity	99.8%;	Pred. No. 1e-286;		
Matches 627; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

Qy	396	GTGGCCATCTCTCCCTTCAAGTAACCTGTGGCCCAAGACTTCTGGGAAGAGACCCCACTGGAACT	455
Db	766	GTGCCATCTCTGCTTCAAGTAACCTGTGGCCCAAGACTTCTGGGAAGAGACCCCACTGGAACT	707
Qy	456	TCGGAAGTAACCTAGTAAGCCCAAGATGGAAGAGTGTAGGGGCTTGGACCACAACGTGT	515
Db	706	TCGGAAGTAACCTAGTAAGCCCAAGATGGAAGAGTGTAGGGGCTTGGACCACAACGTGT	647
Qy	516	CAGTGGAGAGGTCAAGACTCCAGATCACAGGCGCTGTGAGGAGAGCTCATCTTACTAGAC	575
Db	646	CAGTGGAGAGGTCAAGACTCCAGATCACAGGCGCTGTGAGGAGAGCTCATCTTACTAGAC	587
Qy	576	GAGAAGACTTAATACCAACCGCGCTCTCTCTCACACACTCATATCCCGCCCAACGTGTGG	635
Db	586	GAGAAGACTTAATACCAACCGCGCTCTCTCTCACACACTCATATCCCGCCCAACGTGTGG	527
Qy	636	GGCTGACCAATGCAACCTCAATATGGCGCTTCAAGAGGAGAGCCCACTGACTCTCTTCC	695
Db	526	GGCTGACCAATGCAACCTCAATATGGCGCTTCAAGAGGAGAGCCCACTGACTCTCTTCC	467
Qy	696	TTTACCTTATGGCATTTGGCCATATCTCTGTGGGGAAAAATTCTAGTATTTTATT	755
Db	466	TTTACCTTATGGCATTTGGCCATATCTCTGTGGGGAAAAATTCTAGTATTTTATT	407
Qy	756	ATTGATCTTACAGCAACAATATGAGAACTCTGGCCATGAGAGCTTGTACCACTGAA	815
Db	406	ATTGATCTTACAGCAACAATATGAGAACTCTGGCCATGAGAGCTTGTACCACTGAA	347
Qy	816	TCACCAAGCGATACGAACTCTTGCCACACAAAATGTGTGGCAATTAATAATATATCAAG	875
Db	346	TCACCAAGCGATACGAACTCTTGCCACACAAAATGTGTGGCAATTAATAATATATCAAG	287
Qy	876	CAATATATCTCCCAACCAAGGCTTCTTAACGTGGGACCATATATCTCATATAGGCGTGT	935
Db	286	CAATATATCTCCCAACCAAGGCTTCTTAACGTGGGACCATATATCTCATATAGGCGTGT	227

OY	936	TGTGAGATTGACGAATACCCTGGAAAGCCCTAGCAGTGCAGCAATGAGGG	995
Dd	226	TGTGAGCATTTAGAGTAAGAATACTGTGAAGTGCTTAGCGACTGCCAGCAATGAGAG	167
OY	996	CATTCAATGAACATTTTTTTCATATAA	1023
Dd	166	CATTCAATGAACATTTTTTTCATATAA	139
RESULT	3		
B1905842		936 bp	mRNA linear EST 16-OCT-2001
LOCUS			
DEFINITION	603062920P1 NIH_MGC_118 Homo sapiens cdna clone IMAGE:5212085 5'		
ACCESSION	B1905842		
VERSION	B1905842.1	GI:16168433	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 936)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LLM11532 row: h column: 06 High quality sequence start: 5 High quality sequence stop: 861. Location/Qualifiers 1. 936 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="5212085" /clone_id="NIH_MGC_118" /tissue_type="Leukocyte" /lab_host="DH10B" /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb. Insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: This is a NIH_MGC Library."		
BASE COUNT	220 a	268 c	248 g 200 t
ORIGIN			
Query Match	51.6%	Score 553;	DB 10; Length 936;
Best Local Similarity	99.6%;	Pred. No. 2.6e-274;	
Matches 703; Conservative	0;	Mismatches 3;	Indels 0; Gaps 0;
OY	13	TCCGGAACAAGCATTGGGCGGCGAGCGGTGGCACGGCGTGGCTGTGGGGCTGC	72
Dd	9	TCCGGAACAAGCATTGTGGCGGCGACGCTGGCACGGCGTGGCTGTGTGGGCTGC	68
OY	73	GGCCCTGCCGCGAGCAGAGCAAGACTTCTACGACTTCAAGGCGTCAACATCCGGGCAA	132
Dd	69	GGCCCTGCCGCGAGCAGAGCAAGACTTCTACGACTTCAAGGCGTCAACATCCGGGCAA	128
OY	133	ACTGCTGTGCTGGAGAAAGTACCGCGAATCGGTGTCCCTGTGTGAATGTGGCCAGCGA	192

Db	129	ACTGCTGTGCGTGGAGAGTACCGGGGATTCGATGTCCTGTGGTGGTAATGTGGCCACAGCA	188
OY	193	GTGGCGGCTTTCACAGACCAGCACTACCGAGCCCTGTGAGACAGTGCAGCGACACTTGTGGCCC	252
Db	189	GTGGCGGCTTTCACAGACCAGCACTACCGAGCCCTGTGAGAGGTGTGACGACAGACTGTGGGCC	248
OY	253	CCACCACTTTCACAGCGTGTGCGCTTCCCTGTGCAACAGATTTTGGCCAAACAGAGACCTGCAGAG	312
Db	249	CCACCACTTTCACAGCGTGTGCGCTTCCCTGTGCAACAGATTTTGGCCAAACAGAGACCTGCAGAG	308
OY	313	CAACAGAGAGATTTGAGAGCTTTTGCTGTGCGCAGCACTACAGTGTCTCATTTCCCATGTATTAG	372
Db	309	CAACAGAGAGATTTGAGAGCTTTTGCTGTGCGCAGCACTACAGTGTCTCATTTCCCATGTATTAG	368
OY	373	CAAGATTCAGAGTACCGGCTACGTGTGGCCATTCCTGCTTCAAGATTCAGTGGCCGAGACTTC	432
Db	369	CAAGATTCAGAGTACCGGCTACGTGTGGCCATTCCTGCTTCAAGATTCAGTGGCCGAGACTTC	428
OY	433	TGGGAGAGAGCCCACTGTGGAACCTTCTGTGAGTACCTAGAGCCCAAGATGGAAGGTGT	492
Db	429	TGGGAGAGAGCCCACTGTGGAACCTTCTGTGAGTACCTAGAGCCCAAGATGGAAGGTGT	488
OY	493	AGGGCTTGTGGAGCCCAACTGTGTCTAGGTGAGAGGTACAGACTCCAGATCACAGCGCTGT	552
Db	489	AGGGCTTGTGGAGCCCAACTGTGTCTAGGTGAGAGGTACAGACTCCAGATCACAGCGCTGT	548
OY	553	GAGGAGGTCTACTCTACTGGAAGCGAGAGACTTTAAACACACCGCTCTCTCTCTCCACCA	612
Db	549	GAGGAGGTCTACTCTACTGGAAGCGAGAGACTTTAAACACACCGCTCTCTCTCTCCACCA	608
OY	613	CCTCATCCCGCCCACTGTGTGTGGGGCTGACCAAGTCAAACTCAAAATGTGCTTCAAGGG	672
Db	609	ACTCATCCCGCCCACTGTGTGTGGGGCTGACCAAGTCAAACTCAAAATGTGCTTCAAGGG	668
OY	673	AGAGACCCCACTGACTCTCTCTCTTACTCTTATGCCATTTGGTCCC	718
Db	669	AGAGACCCCACTGACTCTCTCTCTTACTCTTATGCCATTTGGTCCC	714
RESULT	4		
LOCUS	B1550170	760 bp	linear EST 05-SEP-2001
DEFINITION	603193057P1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5264151 5',		
ACCESSION	B1550170		
VERSION	B1550170.1	GI:15437482	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L14M1166 row: a column: 16 High quality sequence stop: 750. Location/Qualifiers 1..760 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5264151" /clone_lid="NIH_MGC_95"		
FEATURES			
source			

/tissue_type="hippocampus"
/lab_host="DH108"
/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to Rot 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 160 a 237 c 214 g 149 t
ORIGIN

Query Match 49.5%; Score 531; DB 10; Length 760;
Best Local Similarity 99.7%; Pred. No. 6e-263;
Matches 631; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGCGCGCACCTCGGAAACAGCATGTTGGCGGAGCGGCGCGTGGCTGCT 60
|||||
DB 20 GAGCGCGCACCTCGGAAACAGCATGTTGGCGGAGCGGCGCTGGCTGCT 79
QY 61 CCTGTGGCTGGCGCTCGCGCAGCAGAGAGACTTCTACGACTTCAAGCGGTCAA 120
80 CCTGTGGCTGGCGCTCGCGCAGCAGAGAGACTTCTACGACTTCAAGCGGTCAA 139
QY 121 CATCGGGGCAAACTGTGTCTGAGAGATACCGCGGATGGTGTCTGTTGTA 180
140 CATCGGGGCAAACTGTGTCTGAGAGATACCGCGGATGGTGTCTGTTGTA 199
DB 181 TGTGGCAGCAGAGTGGCTTCACAGACGACTACCGAGCGCTGCGACAGCTGACGC 240
200 TGTGGCAGCAGAGTGGCTTCACAGACGACTACCGAGCGCTGCGACAGCTGACGC 259
QY 241 AGACCTGGGCCCCACCACTTCAAGTGTGCTGCTTCCCTGCAACAGATTGGCCAA 300
260 AGACCTGGGCCCCACCACTTCAAGTGTGCTGCTTCCCTGCAACAGATTGGCCAA 319
DB 301 GGAGCGTGCACAGCAAGAGGATGAGAGCTTGGCTCCGACACTACAGTGTCTATT 360
320 GGAGCGTGCACAGCAAGAGGATGAGAGCTTGGCTCCGACACTACAGTGTCTATT 379
QY 361 CCCCATGTTTACAGATTCAGATCACCGGTACTGTGTGCCATCTCTCAAGTACCT 420
380 CCCCATGTTTACAGATTCAGATCACCGGTACTGTGTGCCATCTCTCAAGTACCT 439
DB 421 GGCCCAAGACTTCTGGAGAGAGCCCACTGGAATCTTGAAGTACTAGTACCCAGA 480
440 GGCCCAAGACTTCTGGAGAGAGCCCACTGGAATCTTGAAGTACTAGTACCCAGA 499
QY 481 TGGAAAGGTGTAGGGGCTTGGAGCCCACTGTCTAGTGAAGAGAGTACAGTCCAGAT 540
500 TGGAAAGGTGTAGGGGCTTGGAGCCCACTGTCTAGTGAAGAGAGTACAGTCCAGAT 559
DB 541 CACAGCGCTGTGAGAGAGCTCATCTACTGAAGCAGAAAGATTAAACCAACCGGTCT 600
560 CACAGCGCTGTGAGAGAGCTCATCTACTGAAGCAGAAAGATTAAACCAACCGGTCT 619
QY 601 CCTCTCCACCACTTCATCCCGCCCACTGTGT 633
620 CCTCTCCACCACTTCATCCCGCCCACTGTGT 652

RESULT 5
AM957082 AM957082 625 bp mRNA linear EST 01-JUN-2000
LOCUS
DEFINITION EST169152 MAGE resequences, MAGD Homo sapiens CDNA, mRNA sequence.
ACCESSION AM957082
VERSION AM957082.1 GI:8146765
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Sneed, A.L., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
TITLE
Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL
Unpublished (2000)
COMMENT
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johng@tigr.org
Plate: 101
Seq primer: Reverse.

FEATURES
source
Location/Qualifiers
1..625
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGD"
/note="Vector: pBluescriptSm"

BASE COUNT 200 a 150 c 127 g 147 t 1 others
ORIGIN

Query Match 48.9%; Score 524; DB 9; Length 625;
Best Local Similarity 100.0%; Pred. No. 2.4e-259;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 535 CCAGATCAGAGCGCTCGTGAGAGAGTCACTCTACTGAAGCAGAAAGCTTTAACCAAC 594
DB 22 CCAGATCAGAGCGCTCGTGAGAGAGTCACTCTACTGAAGCAGAAAGCTTTAACCAAC 81
QY 595 GCGTCTCTCTCCACCACTCATCCGCGCACTGTGGGGGCTGAGCAATGCAATGC 654
DB 82 GCGTCTCTCTCCACCACTCATCCGCGCACTGTGGGGGCTGAGCAATGCAATGC 141
QY 655 AATAGTGTCTTAAGAGGAGAGACCACTGACTCTCTCTCTTACTCTTATGCCATTGG 714
DB 142 AATAGTGTCTTAAGAGGAGAGACCACTGACTCTCTCTCTTACTCTTATGCCATTGG 201
QY 715 TCCCATCATCTTGTGGGGGAAAAATTTAGTATTTTGTATTTGATTTGAATCTTACAGCAAC 774
DB 202 TCCCATCATCTTGTGGGGGAAAAATTTAGTATTTTGTATTTGATTTGAATCTTACAGCAAC 261
QY 775 AATAGGAATCTCTGCGCAATGAGAGCTTGTGACAGTAATCAGCAGCCGATACGAGC 834
DB 262 AATAGGAATCTCTGCGCAATGAGAGCTTGTGACAGTAATCAGCAGCCGATACGAGC 321
QY 835 TCTTGCAACAAAAATGTGTGGCAATAGAGTATATCAAGCAATATCTCCACCAG 894
DB 322 TCTTGCAACAAAAATGTGTGGCAATAGAGTATATCAAGCAATATCTCCACCAG 381
QY 895 GCTTGTGTAACCTGGAGCAATATATCTCAATAGGGGCTGTGTGAGATTGAGATGAAA 954
DB 382 GCTTGTGTAACCTGGAGCAATATATCTCAATAGGGGCTGTGTGAGATTGAGATGAAA 441
QY 955 TACCTGTGAAGAGTGTAGAGAGTGCAGCAAAATAGAGGCAATTCATGAATGAACTTTT 1014
DB 442 TACCTGTGAAGAGTGTAGAGAGTGCAGCAAAATAGAGGCAATTCATGAATGAACTTTT 501
QY 1015 GCATATTAACCAAAAAATTAATCTGTATCAATTAATTAATCTGTGAT 1058
DB 502 GCATATTAACCAAAAAATTAATCTGTATCAATTAATTAATCTGTGAT 545

RESULT 6
BE383506 BE383506 617 bp mRNA linear EST 21-JUL-2000
LOCUS
DEFINITION 601298586F1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:3628580 5', mRNA sequence.

Accession	Version	KeyWords	Source	Organism	Reference	Authors	Title	Journal	Comment
BE383506	1	GI:9328871	EST.	human.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 617)	NIH-MGC http://mgc.nci.nih.gov/	Unpublished (1999)	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC
CDNA Library	Arrayed by: The I.M.A.G.E. Consortium (ULNL)	DNA Sequencing by: Incyte Genomics, Inc.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: image.lnl.gov	Plate: L1C3M33	row: 1	column: 21	High quality sequence start: 7	High quality sequence stop: 617.	Location/Qualifiers
1.	617	/organism="Homo sapiens"	/db_xref="taxon:9606"	/clone="IMAGE:3628580"	/clone_lib="NIH_MGC_19"	/tissue_type="neuroblastoma"	/lab_host="DH10B (phage-resistant)"	/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC Library."	
BASE COUNT	130 a	193 c	178 g	116 t					
ORIGIN									
Query Match	46.8%	Score 502;	DB 10;	Length 617;					
Best Local Similarity	99.7%	Pred. No. 5.6e-248;							
Matches 602;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0					
46	AGCGCGTGGCGCTCTCTGTGGGCTGCGCGCTCGCGCGAGAGAGAGACTTCTACGA	105							
14	AGCGCGTGGCGCTCTCTGTGGGCTGCGCGCTCGCGCGAGAGAGAGACTTCTACGA	73							
106	CTTCAAGCGCGCTCAACATTCGGGGCAAACTGTGTCGTGCTGAGAAAGTACCGGGATCGGT	165							
74	CTTCAAGCGCGCTCAACATTCGGGGCAAACTGTGTCGTGCTGAGAAAGTACCGGGATCGGT	133							
166	GTCCCTGTGGTGAATGTGGCGAGGAGTGGGGCTTACAGACACAGCATACCGAGACCGCT	225							
134	GTCCCTGTGGTGAATGTGGCGAGGAGTGGGGCTTACAGACACAGCATACCGAGACCGCT	193							
226	GCAGCAGCTGCAGCAGACCTTGGGGCCACACACTTCAACGTGCTCCCTCCCGCA	285							
194	GCAGCAGCTGCAGCAGACCTTGGGGCCACACACTTCAACGTGCTCCCTCCCGCA	253							
286	CCAGTTTGGCCCAACAGAGACCTGACACAGCAACAGAGATTGAGAGCTTGGCTGGCGCAC	345							
254	CCAGTTTGGCCCAACAGAGACCTGACACAGCAACAGAGATTGAGAGCTTGGCGCGCAC	313							
346	CTACAGTGTCTATTCCCATGTTTAAAGCAAGATTGACAGTACACGGTACGTGCCATCC	405							
314	CTACAGTGTCTATTCCCATGTTTAAAGCAAGATTGACAGTACACGGTACGTGCCATCC	373							
406	TGCCTTCAAGTACCTGGGCCAGACTTGTGGGAAGAGAGCCACCTGGAACTTGTGAAGTA	465							
374	TGCCTTCAAGTACCTGGGCCAGACTTGTGGGAAGAGAGCCACCTGGAACTTGTGAAGTA	433							

Yy	466	CCTAGTAGCCCCACATGGAAAGTGATAGGGCGCTTGGACACCACCTGTGTAGTGGAGGA	525
Yy	466	CCTAGTAGCCCCACATGGAAAGTGATAGGGCGCTTGGACACCACCTGTGTAGTGGAGGA	525
Db	434	CCTAGTAGCCCCACATGGAAAGTGATAGGGCGCTTGGACACCACCTGTGTAGTGGAGGA	493
Yy	526	GGTAGACTCCAGATTCACAGCGCTCGTAGGAGACCTCATCTCTACTGGAAGCAGAAAGACTT	585
Db	494	GGTAGAGACCCAGATTCACAGCGCTCGTAGGAGACCTCATCTCTACTGGAAGCAGAAAGACTT	553
Yy	586	ATAACACACCGGTCTCCTCTCTCCACACACCTCATCCCGCCACCTGTGTGGGGCTTGACCA	645
Db	554	ATAACACACCGGTCTCCTCTCTCCACACACCTCATCCCGCCACCTGTGTGGGGCTTGACCA	613
Yy	646	TGCA 649	
Db	614	TGCA 617	
RESULT	7		
LOCUS	AA406605/c	519 bp	mRNA linear EST 17-MAY-1997
DEFINITION	AA406605	z15b04.s1 Soares_NHMPu_S1	Homo sapiens cDNA clone IMAGE:75679
ACCESSION	AA406605		
VERSION	AA406605		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 519)		
	Hillier,L., Allen,M., Bowles,L., Dubuque,T., Gelsel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theisling,B., White,T., Wyllie,T., Waterston,R. and Wilson,R.		
	Washu-Merck EST Project 1997		
	Unpublished (1997)		
TITLE	Washington University School of Medicine		
JOURNAL	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
COMMENT	TEL: 314 286 1800		
	Fax: 314 286 1810		
	Email: east@wustl.wustl.edu		
	This clone is available royalty-free through LNL ; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
	Seq primer: -41m3 fwd. Et from Amersham		
	High quality sequence stop: 461.		
FEATURES	Location/Qualifiers		
source	1..519		
	/organism="Homo sapiens"		
	/db_xref="GDB:597654.3"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:753679"		
	/clone_id="Soares_NHMPu_S1"		
	/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"		
	/lab_host="DH10B"		
	/note="Organ: mixed (see below); Vector: p773D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NB19M, pregnant uterus NB19PU, and fetal heart NB1919M) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."		
BASE COUNT	131 a 100 c 126 g 162 t		
ORIGIN			
Query Match	43.7%	Score 468;	DB 9; Length 519;

RESULT 11
 BI561449 846 bp mRNA linear EST 05-SEP-2001
 LOCUS 603256131F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5298607 5',
 DEFINITION mRNA sequence.
 ACCESSION BI561449 GI:15448763
 VERSION BI561449.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM11755 row: m column: 08
 High quality sequence stop: 842.

FEATURES

source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5298607"
 /clone_1ib="NIH_MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to R0F 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."
 BASE COUNT 194 a 244 c 232 g 175 t 1 others

Query Match 40.8%; Score 437; DB 10; Length 846;
 Best Local Similarity 99.5%; Pred. No. 2.2e-214;
 Matches 587; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 19 ACAAGCCATGGTGGGGCGACGCGTGGCGTGGCTGCTGGGGCGGCTG 78
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 Db 9 ACAACCCATGGTGGGGCGACGCGTGGCGTGGCTGCTGGGGCGGCTG 68
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 79 CCGCGACGAGGACGAGACTTCTACGACTTCAAGCGGCTCAACATCCGGGCAACTGGT 138
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 69 CCGCGACGAGGACGAGACTTCTACGACTTCAAGCGGCGTCAACATCCGGGCAACTGGT 128
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 139 GTGCGTAGAAGATACCGCGGATCGGTGTCCTGCTGGTGTGATGTGGCCAGCGATGCGG 198
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 129 ATCGCTGGAAGATACCGCGGATCGGTGTCCTGCTGGTGTGATGTGGCCAGCGATGCGG 188
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 199 CTTCAACAGACGACACTACCGAGCCCTCGACAGCGTGGCGAGACCTGGGCCCCACCA 258
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 189 CTTCAACAGACGACACTACCGAGCCCTCGACAGCGTGGCGAGACCTGGGCCCCACCA 248
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 259 CTTCAACAGCGTGGCTTCCCTCGAACCAAGTTTGGCCAAAGAGAGCTGACGACAA 318
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 249 CTTCAACGTCGCTCCCTCCCTGCAACAGTTTGGCCAAAGAGAGCTGACGACAA 308

QY 319 GGAGATTGAGAGCTTTGGCTGCGCCACCTACAGTGTCTCATTTCCCATGTTTACCAAGAT 378
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 309 GGAGATTGAGAGCTTTGGCGCCCGCCACCTACAGTGTCTCATTTCCCATGTTTACCAAGAT 368
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 379 TGCAGTCAACCGTACTGTGTCGCCATCTGCTTCAAGTACTGGGCCGAGACTTCTGGGAA 438
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 369 TGCAGTCAACCGTACTGTGTCGCCATCTGCTTCAAGTACTGGGCCGAGACTTCTGGGAA 428
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 439 GGAGCCACCTGGAACCTTGGAGTACTAGTACCCCGCAATGGAAAGTGTTAGSGGC 498
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 429 GGAGCCACCTGGAACCTTGGAGTACTAGTACCCCGCAATGGAAAGTGTTAGSGGC 488
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 499 TTGGACCCCAACTGTGTGAGTGGAGAGTCAAGTCCAGATCACAGCGCTGTGAGGAA 558
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 489 TTGGACCCCAACTGTGTGAGTGGAGAGTCAAGTCCAGATCACAGCGCTGTGAGGAA 548
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 559 GCTCATCTTCTAGAACGAGAAAGTATTAACCCAGCGGTCTCCCTGCC 608
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 Db 549 GCTCATCTTCTAGAACGAGAAAGTATTAACCCAGCGGTCTCTCTCC 598

RESULT 12
 AI925364 465 bp mRNA linear EST 08-MAR-2000
 LOCUS wn3c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449158 3',
 DEFINITION mRNA sequence.
 ACCESSION AI925364
 VERSION AI925364
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 465)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

COMMENT
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.lnl.gov/bbrp/image/image.html
 Insert length: 1075 Std Error: 0.00
 Seg primer: -40up from Gibco
 High quality sequence stop: 453.

FEATURES

source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2449158"
 /clone_1ib="NCI_CGAP_Lu19"
 /tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pTZ19-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 121 a 88 c 110 g 146 t

Query Match 39.1%; Score 419; DB 9; Length 465;
Best Local Similarity 100.0%; Pred. No. 4.2e-205;
Matches 419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 CTCACACACCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGGTGTCT 664
DB 461 CTCACACACCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGGTGTCT 402
QY 665 TCAAAAGGAGAGACCCACTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 724
DB 401 TCAAAAGGAGAGACCCACTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 342
QY 725 CTTGGGGGGAATAATTCAGTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 784
DB 341 CTTGGGGGGAATAATTCAGTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 282
QY 785 TCTTGCCCATGAGAGCTCTTGACCAAGTACACAGCCGATACAGCTCTTGCCCAAC 844
DB 281 TCTTGCCCATGAGAGCTCTTGACCAAGTACACAGCCGATACAGCTCTTGCCCAAC 222
QY 845 AAAAATGTGTGCAATATAGATATATCAAGCAATATATCTCCACCCCAAGCTTCTGTAA 904
DB 221 AAAAATGTGTGCAATATAGATATATCAAGCAATATATCTCCACCCCAAGCTTCTGTAA 162
QY 905 ACTGGGACCAATGATTAATCTCATAGGGCTGTGTGAGGATTTAGGATTAATTAATCTGTAA 964
DB 161 ACTGGGACCAATGATTAATCTCATAGGGCTGTGTGAGGATTTAGGATTAATTAATCTGTAA 102
QY 965 AGTGGCTTAGGAGAGTGGCAGCCAAATAGAGAGCAATTCATGAACATTTTTCATATATAA 1023
DB 101 AGTGGCTTAGGAGAGTGGCAGCCAAATAGAGAGCAATTCATGAACATTTTTCATATATAA 43

RESULT 13
AW576111/c 464 bp mRNA linear EST 15-MAR-2000
LOCUS UI-HF-BL0-adb-c-12-0-UI.s1 NIH.MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3060886 3', mRNA sequence.
ACCESSION AW576111 GI:7247650
VERSION AW576111.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 464)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A.
tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
The following repetitive elements were found in this cDNA
sequence:
65-181, >MIR
Seq Primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1..464
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3060886"

/clone_11b="NIH_MGC_37"
/tissue_type="Lymph"
/cell_type="germlinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (UTI)"
/note="Vector: p7773-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 117 a 88 c 101 g 158 t
ORIGIN

Query Match 38.2%; Score 409; DB 9; Length 464;
Best Local Similarity 100.0%; Pred. No. 6.1e-200;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 615 TCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGGTGTCTTCAAGGAG 674
DB 464 TCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGGTGTCTTCAAGGAG 405
QY 675 AGACCACTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 734
DB 404 AGACCACTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 345
QY 735 AAAAATTCAGTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 794
DB 344 AAAAATTCAGTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 285
QY 795 TGAGACTCTTGACAGTGAATCACCAGCCGATACGAGCTCTTGCCCAACAAATGTGT 854
DB 284 TGAGACTCTTGACAGTGAATCACCAGCCGATACGAGCTCTTGCCCAACAAATGTGT 225
QY 855 GGCAAATAGAGATATATCAAGCAATATATCTCCACCCCAAGCTTCTGTAACTGGAGCA 914
DB 224 GGCAAATAGAGATATATCAAGCAATATATCTCCACCCCAAGCTTCTGTAACTGGAGCA 165
QY 915 ATGATTACCGCATAGGGCTGTGTGAGGATTTAGGATTAATTAATCTGTGAAGTGGCTAG 974
DB 164 ATGATTACCGCATAGGGCTGTGTGAGGATTTAGGATTAATTAATCTGTGAAGTGGCTAG 105
QY 975 CAGTGGCAGCCAAATAGAGAGCAATTCATGAACATTTTTCATATATAA 1023
DB 104 CAGTGGCAGCCAAATAGAGAGCAATTCATGAACATTTTTCATATATAA 56

RESULT 14
AA599283 456 bp mRNA linear EST 12-MAY-1999
LOCUS ag35b03.s1 jia bone marrow stroma Homo sapiens cDNA clone
DEFINITION IMAGE:1091501 3', mRNA sequence.
ACCESSION AA599283
VERSION AA599283.1 GI:2432908
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 456)
AUTHORS Jia, L., Robey, P., Young, M., Schuler, G., Powell, J., Yang, L., Lennon
G., Hillier, L., Allen, M., Bowles, L., Geisler, S., Kucaba, T., Marra
M., Martin, J., Stepien, M., Tan, F., Theising, B., Bowers, Y., Wylie
T., Waterston, R., Wilson, R. and Francomano, C.
WashU-MGB/NHGRI EST Project
Unpublished (1997)
Contact: Wilson RK / Jia L
WashU-MGB/NHGRI EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1191 Std Error: 0.00
Seq primer: -40m13 fwd. EF from Amersham
High quality sequence stop: 447.

FEATURES

SOURCE

1. 456
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1091501"
/clone_1lb="Jia bone marrow stroma"
/sex="mixed"
/tissue.type="bone marrow stroma"
/dev_stage="mixed"
/lab_host="XLI-Blue MRF/SOLR"
/note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI;
mRNA made from human bone marrow stroma, cDNA made by
oligo-dT priming. Directionally cloned. Size-selected for
average insert size >0.5 kb. Library supplied by Dr. libin
Jia (NIGRI)."
BASE COUNT 117 a 89 c 106 g 144 t
ORIGIN

Query Match 37.7%; Score 404; DB 9; Length 456;
Best Local Similarity 99.8%; Pred. No. 2.3e-197;
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 608 CACCACTCCTCCTCCGACCTGCTGGGGCTGACCAATGCAAACTCAATGGTCTTCA 667
DB 456 CACCACTCCTCCTCCGACCTGCTGGGGCTGACCAATGCAAACTCAATGGTCTTCA 397
QY 668 AAGGAGAGACCCGACCTCCTCCTTACTCTTATGCAATGGTCCCATCTCTT 727
DB 336 AAGGAGAGACCCGACCTCCTCCTTACTCTTATGCAATGGTCCCATCTCTT 337
QY 728 GTGGGGGAAAAATCTAGTATTTTGAATCTTACGACCAAAATAGGAAGTCC 787
DB 336 GTGGGGGAAAAATCTAGTATTTTGAATCTTACGACCAAAATAGGAAGTCC 277
QY 788 TGGCCCAATGAGCTCTTGACCAATGATCACCAGCCGATGACAGCTTGGCAACAA 847
DB 276 TGGCCCAATGAGCTCTTGACCAATGATCACCAGCCGATGACAGCTTGGCAACAA 217
QY 848 AATGTGTGCAATGAAATATATATCAAGCAATATCTCCACCAAGCTTGTGTAAT 907
DB 216 AATGTGTGCAATGAAATATATATCAAGCAATATCTCCACCAAGCTTGTGTAAT 157
QY 908 GAGCAATGATTAATCTCATAGGCTGTTGTGAGATTAAGATGAATACCTGTGAAGT 967
DB 156 GAGCAATGATTAATCTCATAGGCTGTTGTGAGATTAAGATGAATACCTGTGAAGT 97
QY 968 GCGTAGGCGCTGCGACGCAATAGAGGAGCATCAATGAACATTTTTCATATAACCA 1027
DB 96 GCGTAGGCGCTGCGACGCAATAGAGGAGCATCAATGAACATTTTTCATATAACCA 37
QY 1028 AAAATTAATCTGTTATCAATAAAACTTGATCCAA 1062
DB 36 AAAATTAATCTGTTATCAATAAAACTTGATCCAA 2

RESULT 15
AI332841 466 bp mRNA linear EST 13-FEB-1999
LOCUS AI332841/c
DEFINITION qp96g11.x1 Soares_fetal_lung NBHL19W Homo sapiens cDNA clone
IMAGE:1930916 3', mRNA sequence.
ACCESSION AI332841
VERSION AI332841.1 GI:4069400
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

1 (bases 1 to 466)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

COMMENT

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1446 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 394.

FEATURES

SOURCE

1. 466
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1930916"
/clone_1lb="Soares_fetal_lung_NBHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-GTGACCAATCTGAAGTGGAGGCGCGCAATTTTGTGTTTGT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Patricia Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."
BASE COUNT 122 a 91 c 102 g 151 t
ORIGIN

Query Match 37.3%; Score 400; DB 9; Length 466;
Best Local Similarity 100.0%; Pred. No. 2.7e-195;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 624 CCACCTGTGGGGGCTGACCAATGCAAACTCAATGATGCTTCAAGGAGACCCACT 683
DB 466 CCACCTGTGGGGGCTGACCAATGCAAACTCAATGATGCTTCAAGGAGACCCACT 407
QY 684 GACTCTCCTCTTCTTACTCTTATGACCATTTGTCATCTTGTGGGAAAAATTC 743
DB 406 GACTCTCCTCTTCTTACTCTTATGACCATTTGTCATCTTGTGGGAAAAATTC 347
QY 744 AGTATTTTGAATTTTGAATCTTACGCAAAATAGGAAGCTCCGCAATGAGCTC 803
DB 346 AGTATTTTGAATTTTGAATCTTACGCAAAATAGGAAGCTCCGCAATGAGCTC 287
QY 804 TTGACCAATGCAATCACCAGCGATAGCAAGCTTTCACCAAAAAATGTTGGCAATAG 863
DB 286 TTGACCAATGCAATCACCAGCGATAGCAAGCTTTCGCAAAAAATGTTGGCAATAG 227
QY 864 AAGTATATCAAGCAATATCTCCACCAAGCTTGTGTAATGGAGCAATGATTAC 923
DB 226 AAGTATATCAAGCAATATCTCCACCAAGCTTGTGTAATGGAGCAATGATTAC 167
QY 924 TCATAGGCGCTGTGTGAGGATTAAGATGAATACCTGTGAAGCTAGGCGTGCAG 983
DB 166 TCATAGGCGCTGTGTGAGGATTAAGATGAATACCTGTGAAGCTAGGCGTGCAG 107
QY 984 CCAATATAGGAGCATCAATGATGATTTTTCATATAA 1023
DB 106 CCAATATAGGAGCATCAATGATGATTTTTCATATAA 67

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